Page 6, please delete the first full paragraph, and replace it with the following new paragraph:

D2

Figure 3 lists the sequence-specific zinc finger clones (SEQ ID NOS: 15-109, respectively in order of appearance) obtained from phage selections, and their binding site signatures.

Page 6, please delete the third paragraph, and replace it with the following new paragraph:

D3

Figure 5, illustrates the sequence-specific interactions selected for at position 2 of the α-helix, binding to position 1 of the quadruplet (SEQ ID NOS: 74, 73, 54, 15-16, 57-58, 70, 73, 75, 45, 67, 105, 84, 76, 77, 48, 38 41 and 65-66, respectively, in order of appearance).

D4

Page 6, please delete the fourth paragraph, and replace it with the following new paragraph:

Figure 6 illustrates the design of a zinc finger binding protein (SEQ ID NOS: 110-114, respectively, in order of appearance) specific for a G12V mutant ras oncogene;

Page 10, please delete the fifth full paragraph beginning at line 20 and replace it with the following new paragraph:

D5

Preferably, X_{2-3} is G-K-A, G-K-C, G-K-S or G-K-G. However, departures from the preferred residues are possible, for example in the form of M-R-N (SEQ ID NO: 4) or (SEQ ID NO: 5) M-R.

Page 12, please delete the third paragraph, and replace it with the following new paragraph:

D6

Consensus zinc finger structures may be prepared by comparing the sequences of known zinc fingers, irrespective of whether their binding domain is known. Preferably, the consensus structure is selected from the group consisting of the consensus structure (SEQ ID NO: 6) P Y K C P E C G K S F S Q K S D L V K H Q R T H T G (SEQ ID NO: 5), and the consensus structure (SEQ ID NO: 7) P Y K C S E C G K A F S Q K S N L T R H Q R I H T G E K P (SEQ ID NO: 6).

Page 12, please delete the fourth paragraph, and replace it with the following new paragraph:

D7

The consensuses are derived from the consensus provided by Krizek et al., (1991) J. Am. Chem. Soc. 113:4518-4523 and from Jacobs, (1993) PhD thesis, University of Cambridge, UK. In both cases, the linker sequences described above for joining two zinc finger motifs together, namely TGEK (SEQ ID NO: 4) or TGEKP (SEQ ID NO: 5) can be formed on the ends of the consensus. Thus, a P may be removed where necessary, or, in the case of the consensus terminating T G, E K (P) can be added.

Page 13, please delete the third paragraph, and replace it with the following new paragraph:

D8

A "leader" peptide may be added to the N-terminal finger. Preferably, the leader peptide is (SEQ ID NO: 8) MAEEKP.

Page 35, please delete the second paragraph, and replace it with the following new paragraph:

D9

The first finger of the designer lead peptide is designed according to the rules set forth herein starting from a Zif268 finger 2 model to bind the quadruplet 5' -GCCG-3', which corresponds to 'anticodon' 10 of the designated binding site plus one 3' base. The finger has the following sequence (SEQ ID NO: 9):

Page 35, please delete the fifth paragraph, and replace it with the following new paragraph:

D10

Given the similarity of the DNA subsites, the second and third fingers of the DNA-binding domain are direct repeats of this first finger, but in which the third α-helical residue which contacts base 3 of a quadruplet, +3, is mutated according to recognition rules, to histidine in finger 2 and asparagine in finger 3, such that the specificity of these fingers is predicted to be 5'-GGCG-3' (includes 'anticodon' 11) and 5'-GACG-3' (includes 'anticodon' 12) respectively. Thus the second and third finger polypeptides have the sequences SEQ ID NOS: 10 and 11, respectively)

Page 36, please delete the first paragraph, beginning at line 5, and replace it with the following new paragraph:

D11

A construct consisting of DNA sequences encoding the three fingers joined together, preceded by a leader MAEEKP (SEQ ID NO: 8) at the N-terminus, is cloned as a fusion to the minor coat protein (gene III) of bacteriophage Fd in the phage vector Fd-Tet-SN (Y. Choo, A. Klug, (1994) *Proc. Natl. Acad. Sci. U.S.A.* 91, 11163-11167). In phage display screening K_d of 17nM, and to discriminate strongly against the wild-type sequence.

Please delete original pages 42 - 44 and replace with the new sequence pages 42 -70.